

SEQUENCE LISTING

<110> The Government of the United States of America, as
represented by the Secretary of the Department of Health and
Human Services
Flomerfelt, Francis
Gress, Ronald

<120> SPATIAL FOR ALTERING CELL PROLIFERATION

<130> 4239-64851

<160> 7

<170> PatentIn version 3.2

<210> 1

<211> 933

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (84)..(677)

<223> Coding sequence

<400> 1

```

tcttgagggtt gccaatTTTT tttttttttt tttttttttt tttttttttt ggtttgggga      60
gaaacttggtg ttggaaccag ccc ctg ttt ctg ggg aat gta tat aag ggg agt      113
                Leu Phe Leu Gly Asn Val Tyr Lys Gly Ser
                1                5                10

tta gca cct cgt agg gat gag gtg act agt cca aag gca gag ccc cag      161
Leu Ala Pro Arg Arg Asp Glu Val Thr Ser Pro Lys Ala Glu Pro Gln
                15                20                25

cca gag acg aag ccg gag aac ctt cca agg agc cac ggg gat gtt ggg      209
Pro Glu Thr Lys Pro Glu Asn Leu Pro Arg Ser His Gly Asp Val Gly
                30                35                40

ctc cag aaa gag act gtg gtc cca ggc att gtg gat ttc gag ctg atc      257
Leu Gln Lys Lys Glu Thr Val Val Pro Gly Ile Val Asp Phe Glu Leu Ile
                45                50                55

cat gag gag ctg aag acc aca aag ccc caa aca tca caa cca aca ccc      305
His Glu Glu Leu Lys Thr Thr Lys Pro Gln Thr Ser Gln Pro Thr Pro
                60                65                70

agt gcc tac cgc ttt gga cgc cta agc cac cat tcc ttc ttc tcg agg      353
Ser Ala Tyr Arg Phe Gly Arg Leu Ser His His Ser Phe Phe Ser Arg
                75                80                85                90

cac cac ccc caa cca cag cga gtg act cat atc caa gat atc gct ggg      401
His His Pro Gln Pro Gln Arg Val Thr His Ile Gln Asp Ile Ala Gly
                95                100                105

aag cct gtc tgc gtg gtc agg gac gag ttc tct ctg tcg gcc ttg act      449
Lys Pro Val Cys Val Val Arg Asp Glu Phe Ser Leu Ser Ala Leu Thr
                110                115                120

```

cag ccc aca ttc tta tcc cgc tgt ctg atg ggg atg ccc acc atc tct 497
 Gln Pro Thr Phe Leu Ser Arg Cys Leu Met Gly Met Pro Thr Ile Ser
 125 130 135
 gtc ccc att ggg gat cca cag tcc aat cgg aac ccc cag ctt tct act 545
 Val Pro Ile Gly Asp Pro Gln Ser Asn Arg Asn Pro Gln Leu Ser Thr
 140 145 150
 tct gac acc tgg agg aag aaa ctg aag gac ctg gct tcc cga gtg act 593
 Ser Asp Thr Trp Arg Lys Lys Leu Lys Asp Leu Ala Ser Arg Val Thr
 155 160 165 170
 gtc ttc act aag gaa atc cag cca aag ccc gat gag gtt ggt gtt gca 641
 Val Phe Thr Lys Glu Ile Gln Pro Lys Pro Asp Glu Val Gly Val Ala
 175 180 185
 caa aga atg gag cct aga aaa aaa agg cct tct taa gtctccccaa 687
 Gln Arg Met Glu Pro Arg Lys Lys Arg Pro Ser
 190 195
 tgctcagctg ctggcacggg aggggaagga ccctcataac ctggaagggtg acagcgaaaa 747
 tcaaagaaac acaaaatcac acctagcaga gaaatccaag aagggttccc agaaacaccc 807
 tctaaagcaa ctgttcccaa cctgttctaatt gccttgaccc ttgaatacag tttctcacac 867
 tgcagtaacc cctgcccccg aaataaaaatt attttcatta ctacttcaaa aaaaaaaaaa 927
 aaaaaa 933

<210> 2
 <211> 197
 <212> PRT
 <213> Mus musculus

<400> 2

Leu Phe Leu Gly Asn Val Tyr Lys Gly Ser Leu Ala Pro Arg Arg Asp
 1 5 10 15

Glu Val Thr Ser Pro Lys Ala Glu Pro Gln Pro Glu Thr Lys Pro Glu
 20 25 30

Asn Leu Pro Arg Ser His Gly Asp Val Gly Leu Gln Lys Glu Thr Val
 35 40 45

Val Pro Gly Ile Val Asp Phe Glu Leu Ile His Glu Glu Leu Lys Thr
 50 55 60

Thr Lys Pro Gln Thr Ser Gln Pro Thr Pro Ser Ala Tyr Arg Phe Gly
 65 70 75 80

Arg Leu Ser His His Ser Phe Phe Ser Arg His His Pro Gln Pro Gln
 85 90 95

Arg Val Thr His Ile Gln Asp Ile Ala Gly Lys Pro Val Cys Val Val
 100 105 110

Arg Asp Glu Phe Ser Leu Ser Ala Leu Thr Gln Pro Thr Phe Leu Ser
 115 120 125

Arg Cys Leu Met Gly Met Pro Thr Ile Ser Val Pro Ile Gly Asp Pro
 130 135 140

Gln Ser Asn Arg Asn Pro Gln Leu Ser Thr Ser Asp Thr Trp Arg Lys
 145 150 155 160

Lys Leu Lys Asp Leu Ala Ser Arg Val Thr Val Phe Thr Lys Glu Ile
 165 170 175

Gln Pro Lys Pro Asp Glu Val Gly Val Ala Gln Arg Met Glu Pro Arg
 180 185 190

Lys Lys Arg Pro Ser
 195

<210> 3
 <211> 1035
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (84)..(779)
 <223> Coding sequence

<400> 3
 tcttgagggt gccaatTTTT tttttttttt tttttttttt tttttttttt ggtttgggga 60
 gaaacttggtg ttggaaccag ccc ctg ttt ctg ggg aat gta tat aag ggg agt 113
 Leu, Phe Leu Gly Asn Val Tyr Lys Gly Ser
 1 5 10
 tta gca cct cgt agg gat gag gtg act agt cca aag gca gag ccc cag 161
 Leu Ala Pro Arg Arg Asp Glu Val Thr Ser Pro Lys Ala Glu Pro Gln
 15 20 25
 cca gag acg aag ccg gag aac ctt cca agg agc cac ggg gat gtt ggg 209
 Pro Glu Thr Lys Pro Glu Asn Leu Pro Arg Ser His Gly Asp Val Gly
 30 35 40
 ctc cag aaa gag act gtg gtc cca ggc att gtg gat ttc gag ctg atc 257
 Leu Gln Lys Glu Thr Val Val Pro Gly Ile Val Asp Phe Glu Leu Ile
 45 50 55
 cat gag gag ctg aag acc aca aag ccc caa aca tca caa cca aca ccc 305

| | | | | | | | | | | | | | | | | | |
|--|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| His | Glu | Glu | Leu | Lys | Thr | Thr | Lys | Pro | Gln | Thr | Ser | Gln | Pro | Thr | Pro | | |
| 60 | | | | | | 65 | | | | | 70 | | | | | | |
| agt gcc tac cgc ttt gga cgc cta agc cac cat tcc ttc ttc tcg agg | | | | | | | | | | | | | | | | | 353 |
| Ser Ala Tyr Arg Phe Gly Arg Leu Ser His His Ser Phe Phe Ser Arg | | | | | | | | | | | | | | | | | |
| 75 | | | | | 80 | | | | 85 | | | | | | | 90 | |
| cac cac ccc caa cca cag cga gtg act cat atc caa gtt aca gga aga | | | | | | | | | | | | | | | | | 401 |
| His His Pro Gln Pro Gln Arg Val Thr His Ile Gln Val Thr Gly Arg | | | | | | | | | | | | | | | | | |
| | | | | 95 | | | | | 100 | | | | | | | 105 | |
| gag gac ctg gag cac tcc ctg ccc ctc acc acc tct ttc cag ctc ctt | | | | | | | | | | | | | | | | | 449 |
| Glu Asp Leu Glu His Ser Leu Pro Leu Thr Thr Ser Phe Gln Leu Leu | | | | | | | | | | | | | | | | | |
| | | | 110 | | | | | 115 | | | | | 120 | | | | |
| caa gct cct ggg gtc cag ccc atg gat ctc act ccc tct gca gat atc | | | | | | | | | | | | | | | | | 497 |
| Gln Ala Pro Gly Val Gln Pro Met Asp Leu Thr Pro Ser Ala Asp Ile | | | | | | | | | | | | | | | | | |
| | | 125 | | | | | 130 | | | | | 135 | | | | | |
| gct ggg aag cct gtc tgc gtg gtc agg gac gag ttc tct ctg tcg gcc | | | | | | | | | | | | | | | | | 545 |
| Ala Gly Lys Pro Val Cys Val Val Arg Asp Glu Phe Ser Leu Ser Ala | | | | | | | | | | | | | | | | | |
| | 140 | | | | | 145 | | | | | 150 | | | | | | |
| ttg act cag ccc aca ttc tta tcc cgc tgt ctg atg ggg atg ccc acc | | | | | | | | | | | | | | | | | 593 |
| Leu Thr Gln Pro Thr Phe Leu Ser Arg Cys Leu Met Gly Met Pro Thr | | | | | | | | | | | | | | | | | |
| | 155 | | | | 160 | | | | 165 | | | | | | | 170 | |
| atc tct gtc ccc att ggg gat cca cag tcc aat cgg aac ccc cag ctt | | | | | | | | | | | | | | | | | 641 |
| Ile Ser Val Pro Ile Gly Asp Pro Gln Ser Asn Arg Asn Pro Gln Leu | | | | | | | | | | | | | | | | | |
| | | | 175 | | | | | 180 | | | | | | | | 185 | |
| tct act tct gac acc tgg agg aag aaa ctg aag gac ctg gct tcc cga | | | | | | | | | | | | | | | | | 689 |
| Ser Thr Ser Asp Thr Trp Arg Lys Lys Leu Lys Asp Leu Ala Ser Arg | | | | | | | | | | | | | | | | | |
| | | 190 | | | | | 195 | | | | | | 200 | | | | |
| gtg act gtc ttc act aag gaa atc cag cca aag ccc gat gag gtt ggt | | | | | | | | | | | | | | | | | 737 |
| Val Thr Val Phe Thr Lys Glu Ile Gln Pro Lys Pro Asp Glu Val Gly | | | | | | | | | | | | | | | | | |
| | 205 | | | | | 210 | | | | | | 215 | | | | | |
| gtt gca caa aga atg gag cct aga aaa aaa agg cct tct taa | | | | | | | | | | | | | | | | | 779 |
| Val Ala Gln Arg Met Glu Pro Arg Lys Lys Arg Pro Ser | | | | | | | | | | | | | | | | | |
| | 220 | | | | | 225 | | | | | 230 | | | | | | |
| gtctccccaa tgctcagctg ctggcacggg aggggaagga ccctcataac ctccaaggtg | | | | | | | | | | | | | | | | | 839 |
| acagcgaaaa tcaaagaaac acaaaatcac acctagcaga gaaatccaag aagggttccc | | | | | | | | | | | | | | | | | 899 |
| agaaacacccc tctaaagcaa ctgttcccaa cctgttctaata gccttgaccc ttgaatacag | | | | | | | | | | | | | | | | | 959 |
| tttctcacac tgcagtaacc cctgcccccg aaataaaatt attttcatta ctacttcaaa | | | | | | | | | | | | | | | | | 1019 |
| aaaaaaaaaa aaaaaa | | | | | | | | | | | | | | | | | 1035 |

<210> 4
 <211> 231
 <212> PRT
 <213> Mus musculus
 <400> 4

Leu Phe Leu Gly Asn Val Tyr Lys Gly Ser Leu Ala Pro Arg Arg Asp
 1 5 10 15
 Glu Val Thr Ser Pro Lys Ala Glu Pro Gln Pro Glu Thr Lys Pro Glu
 20 25 30
 Asn Leu Pro Arg Ser His Gly Asp Val Gly Leu Gln Lys Glu Thr Val
 35 40 45
 Val Pro Gly Ile Val Asp Phe Glu Leu Ile His Glu Glu Leu Lys Thr
 50 55 60
 Thr Lys Pro Gln Thr Ser Gln Pro Thr Pro Ser Ala Tyr Arg Phe Gly
 65 70 75 80
 Arg Leu Ser His His Ser Phe Phe Ser Arg His His Pro Gln Pro Gln
 85 90 95
 Arg Val Thr His Ile Gln Val Thr Gly Arg Glu Asp Leu Glu His Ser
 100 105 110
 Leu Pro Leu Thr Thr Ser Phe Gln Leu Leu Gln Ala Pro Gly Val Gln
 115 120 125
 Pro Met Asp Leu Thr Pro Ser Ala Asp Ile Ala Gly Lys Pro Val Cys
 130 135 140
 Val Val Arg Asp Glu Phe Ser Leu Ser Ala Leu Thr Gln Pro Thr Phe
 145 150 155 160
 Leu Ser Arg Cys Leu Met Gly Met Pro Thr Ile Ser Val Pro Ile Gly
 165 170 175
 Asp Pro Gln Ser Asn Arg Asn Pro Gln Leu Ser Thr Ser Asp Thr Trp
 180 185 190
 Arg Lys Lys Leu Lys Asp Leu Ala Ser Arg Val Thr Val Phe Thr Lys
 195 200 205
 Glu Ile Gln Pro Lys Pro Asp Glu Val Gly Val Ala Gln Arg Met Glu
 210 215 220
 Pro Arg Lys Lys Arg Pro Ser
 225 230

<210> 5

| | |
|---|------|
| gct tgt att gag tgc act ctg gaa ctt tac cca cca cag gtc aat ttc Ala Cys Ile Glu Cys Thr Leu Glu Leu Tyr Pro Pro Gln Val Asn Phe 200 205 210 | 678 |
| ccc atg tgt acc att gca tct atg ccy agg ctc cca gaa cac tgt atc Pro Met Cys Thr Ile Ala Ser Met Xaa Arg Leu Pro Glu His Cys Ile 215 220 225 | 726 |
| gag tat gtg agg atg ttg caa tgg cct aaa gag cag cct ttt gga gat Glu Tyr Val Arg Met Leu Gln Trp Pro Lys Glu Gln Pro Phe Gly Asp 230 235 240 245 | 774 |
| ggg gtt cca tta gat gga gat gac cct gaa cat att cag tgg att ttc Gly Val Pro Leu Asp Gly Asp Asp Pro Glu His Ile Gln Trp Ile Phe 250 255 260 | 822 |
| caa aag tcc ata gag aga gca tca caa tat aat att aga ggc gtt acc Gln Lys Ser Ile Glu Arg Ala Ser Gln Tyr Asn Ile Arg Gly Val Thr 265 270 275 | 870 |
| tac aga ctc act caa ggg gtg gta aaa cga atc att cct gca gta gct Tyr Arg Leu Thr Gln Gly Val Val Lys Arg Ile Ile Pro Ala Val Ala 280 285 290 | 918 |
| tct aca aat gca gtc att gca gct gtg tgt gcc act gag gtt ttc aag Ser Thr Asn Ala Val Ile Ala Ala Val Cys Ala Thr Glu Val Phe Lys 295 300 305 | 966 |
| ata gct aca agt gcg tac att ccc ctt aat aac tac ctg gta ttc aat Ile Ala Thr Ser Ala Tyr Ile Pro Leu Asn Asn Tyr Leu Val Phe Asn 310 315 320 325 | 1014 |
| gat gta gat ggg ctg tac act tac acg ttt gaa gca gag aga aag gaa Asp Val Asp Gly Leu Tyr Thr Tyr Thr Phe Glu Ala Glu Arg Lys Glu 330 335 340 | 1062 |
| aac tgt cca gca tgt agc caa ctt cct caa aac att cag ttt tcc cca Asn Cys Pro Ala Cys Ser Gln Leu Pro Gln Asn Ile Gln Phe Ser Pro 345 350 355 | 1110 |
| tca gct aaa cta cag gag gtc tta gac tac cta acc aac agt gct tct Ser Ala Lys Leu Gln Glu Val Leu Asp Tyr Leu Thr Asn Ser Ala Ser 360 365 370 | 1158 |
| ctg caa atg aag tct ccg gct atc aca gcc aca tta gag ggg aag aac Leu Gln Met Lys Ser Pro Ala Ile Thr Ala Thr Leu Glu Gly Lys Asn 375 380 385 | 1206 |
| agg aca ctt tac tta cag tca gta acg tct att gaa gaa cga acc agg Arg Thr Leu Tyr Leu Gln Ser Val Thr Ser Ile Glu Glu Arg Thr Arg 390 395 400 405 | 1254 |
| ccc aat ctt tcc aaa aca tta aaa gaa ctg gga cta gtt gat gga caa Pro Asn Leu Ser Lys Thr Leu Lys Glu Leu Gly Leu Val Asp Gly Gln 410 415 420 | 1302 |
| gaa ctg gct gtt gct gat gtc act aca cca cag act gta cta ttc aaa Glu Leu Ala Val Ala Asp Val Thr Thr Pro Gln Thr Val Leu Phe Lys 425 430 435 | 1350 |

ctt cat ttt act taa ggaaaataaa tctgcacata atagaaaatt catagaaata 1405
 Leu His Phe Thr
 440

atatacttta taaatgatat gaaattgaag agcctggaag atgaggcaga ggggaacatc 1465
 caagaaagga aatttaattg gtgtcatttt tagcattagt gtggctagaa tttgactttt 1525
 atatatatac atatatataa aaaaggactg actctttttt aactttataa gtttctcttg 1585
 aagactgaac tttgggggtg ggctagcaag cattttcatt ttattactat ggaaagctat 1645
 gccttcagga gagattatga acaagtgtgt tgcttcttta aagcaggaca aacactgtct 1705
 tgtgtgtgag tttgttgtgg tcaaagagca tttcctcag cgtgtatctg aaatccacat 1765
 gtgtagaaat gtctcctggg atggaaatga ggagctatgt ctgaagaata gtaaataatc 1825
 acagcctgac atctagagta tatcaaacat aggcagtgtc ttcattgcta ctcatataat 1885
 tgtgactatc catgtgtgta ttaattattg cagaatttaa cttgtccatg ataatttgta 1945
 aacagtatta tagattcata cctgtgcatg aaaatacaaa atattttcat gtatttgttt 2005
 gcaatgccac agagaccagt atgcacaaat ttaaaccaag acatggctgt tcaaagaaaa 2065
 ttaatgttta aacagttatc attgatgctt ttgcactatt tattaataaa at 2117

<210> 6
 <211> 441
 <212> PRT
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (99)..(99)
 <223> The 'Xaa' at location 99 stands for Val.

<220>
 <221> misc_feature
 <222> (121)..(121)
 <223> The 'Xaa' at location 121 stands for Val.

<220>
 <221> misc_feature
 <222> (127)..(127)
 <223> The 'Xaa' at location 127 stands for Ile.

<220>
 <221> misc_feature
 <222> (222)..(222)
 <223> The 'Xaa' at location 222 stands for Pro.

<400> 6

Met Ala Val Asp Gly Gly Cys Gly Asp Thr Gly Asp Trp Glu Gly Arg
 1 5 10 15

Trp Asn His Val Lys Lys Phe Leu Glu Arg Ser Gly Pro Phe Thr His

| 20 | | | | | | | | | | 25 | | | | | 30 | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| Pro | Asp | Phe | Glu | Pro | Ser | Thr | Glu | Ser | Leu | Gln | Phe | Leu | Leu | Asp | Thr | | | | | | | | | | | | | | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | | | | | | | | | | | | | | |
| Cys | Lys | Val | Leu | Val | Ile | Gly | Ala | Gly | Gly | Leu | Gly | Cys | Glu | Leu | Leu | | | | | | | | | | | | | | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | | | | | | | | | | | | | | |
| Lys | Asn | Leu | Ala | Leu | Ser | Gly | Phe | Arg | Gln | Ile | His | Val | Ile | Asp | Met | | | | | | | | | | | | | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | | | | | | | | | | | | | | |
| Asp | Thr | Ile | Asp | Val | Ser | Asn | Leu | Asn | Arg | Gln | Phe | Leu | Phe | Arg | Pro | | | | | | | | | | | | | | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | | | | | | | | | | | | | | |
| Lys | Asp | Xaa | Gly | Arg | Pro | Lys | Ala | Glu | Val | Ala | Ala | Glu | Phe | Leu | Asn | | | | | | | | | | | | | | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | | | | | | | | | | | | | | |
| Asp | Arg | Val | Pro | Asn | Cys | Asn | Val | Xaa | Pro | His | Phe | Asn | Lys | Xaa | Gln | | | | | | | | | | | | | | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | | | | | | | | | | | | | | |
| Asp | Phe | Asn | Asp | Thr | Phe | Tyr | Arg | Gln | Phe | His | Ile | Ile | Val | Cys | Gly | | | | | | | | | | | | | | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | | | | | | | | | | | | | | |
| Leu | Asp | Ser | Ile | Ile | Ala | Arg | Arg | Trp | Ile | Asn | Gly | Met | Leu | Ile | Ser | | | | | | | | | | | | | | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | | | | | | | | | | | | | | |
| Leu | Leu | Asn | Tyr | Glu | Asp | Gly | Val | Leu | Asp | Pro | Ser | Ser | Ile | Val | Pro | | | | | | | | | | | | | | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | | | | | | | | | | | | | | |
| Leu | Ile | Asp | Gly | Gly | Thr | Glu | Gly | Phe | Lys | Gly | Asn | Ala | Arg | Val | Ile | | | | | | | | | | | | | | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | | | | | | | | | | | | | | |
| Leu | Pro | Gly | Met | Thr | Ala | Cys | Ile | Glu | Cys | Thr | Leu | Glu | Leu | Tyr | Pro | | | | | | | | | | | | | | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | | | | | | | | | | | | | | |
| Pro | Gln | Val | Asn | Phe | Pro | Met | Cys | Thr | Ile | Ala | Ser | Met | Xaa | Arg | Leu | | | | | | | | | | | | | | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | | | | | | | | | | | | | | |
| Pro | Glu | His | Cys | Ile | Glu | Tyr | Val | Arg | Met | Leu | Gln | Trp | Pro | Lys | Glu | | | | | | | | | | | | | | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | | | | | | | | | | | | | | |
| Gln | Pro | Phe | Gly | Asp | Gly | Val | Pro | Leu | Asp | Gly | Asp | Asp | Pro | Glu | His | | | | | | | | | | | | | | | |
| | | | 245 | | | | | | 250 | | | | | 255 | | | | | | | | | | | | | | | | |
| Ile | Gln | Trp | Ile | Phe | Gln | Lys | Ser | Ile | Glu | Arg | Ala | Ser | Gln | Tyr | Asn | | | | | | | | | | | | | | | |
| | | 260 | | | | | | 265 | | | | | 270 | | | | | | | | | | | | | | | | | |

Ile Arg Gly Val Thr Tyr Arg Leu Thr Gln Gly Val Val Lys Arg Ile
 275 280 285

Ile Pro Ala Val Ala Ser Thr Asn Ala Val Ile Ala Ala Val Cys Ala
 290 295 300

Thr Glu Val Phe Lys Ile Ala Thr Ser Ala Tyr Ile Pro Leu Asn Asn
 305 310 315 320

Tyr Leu Val Phe Asn Asp Val Asp Gly Leu Tyr Thr Tyr Thr Phe Glu
 325 330 335

Ala Glu Arg Lys Glu Asn Cys Pro Ala Cys Ser Gln Leu Pro Gln Asn
 340 345 350

Ile Gln Phe Ser Pro Ser Ala Lys Leu Gln Glu Val Leu Asp Tyr Leu
 355 360 365

Thr Asn Ser Ala Ser Leu Gln Met Lys Ser Pro Ala Ile Thr Ala Thr
 370 375 380

Leu Glu Gly Lys Asn Arg Thr Leu Tyr Leu Gln Ser Val Thr Ser Ile
 385 390 395 400

Glu Glu Arg Thr Arg Pro Asn Leu Ser Lys Thr Leu Lys Glu Leu Gly
 405 410 415

Leu Val Asp Gly Gln Glu Leu Ala Val Ala Asp Val Thr Thr Pro Gln
 420 425 430

Thr Val Leu Phe Lys Leu His Phe Thr
 435 440

<210> 7

<211> 5807

<212> DNA

<213> Mus musculus

<400> 7

| | |
|---|-----|
| ttaggtgtcc tagttagggt tactattgac atgatgaaag accgtgacca aagcaactta | 60 |
| aggaggaaag gctttatttg gcttacactt ccataccaca gctcaccatc aaaggaatca | 120 |
| aagggagtca gggcaggaac ctggaggcaa gagctgatgc agaagccatg gaaagatgct | 180 |
| gcttcctage ttgctcccc ttgcttgctc agctggcttt cttgctcagc tccgaggtga | 240 |
| ctccaccctt cctctaccaa tcattaatta ggaaaatgcc taacaggctt ctctacagcc | 300 |

| | |
|--|------|
| ccatcttaag gaagcctttt ctcaagtgag gctccctcct ctccaatgac tttagctggc | 360 |
| attaaattga cataaaacta gccagcacag ggctgaccag ctgagctgcc acccaggccc | 420 |
| gggactcaag gctttgagtt ggcccacccc caaatctaca tcatctgtga actgttgggg | 480 |
| catgtgaaaa tgctgtgcct gttgattcaa agctacatgg tctccatgac acagggtgac | 540 |
| aacgagatat ctgagagggtg tcccaatgag gatctaata t gatggagtc acagaagcca | 600 |
| gacaccttga accaaactaa tgactcattg caatgaatat ttgcaagtga agatgtgtgg | 660 |
| acagaggggtt atactgtggg atatactgta acacattaca tcttccacga tgttttcttt | 720 |
| tctctctttc tctctctctc tctctctctc tctctctctc tctctctctc tctctctctc | 780 |
| tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgttattt gaggaggggt | 840 |
| tgcaggggca gagggcagat atgaggggat gagctggact ggggtgcctg atgtgaaaca | 900 |
| aagaatcaat aaaatgttaa tacaaaggcc cggagagatg gcttagcagt taagagcacc | 960 |
| aactgctctt ccaaagggtcc tgagttcaaa tcccagcaac cacatggtgg ctcaaacca | 1020 |
| tccataatga gatctgacat cctcttcttg gatgtctaaa gatagctaca gtgtacttac | 1080 |
| atataataaa taaatgaatc tttcggctgg agcaagcagg gctggagaga gaagaggtgg | 1140 |
| tgtctgaaga cagctatagt gtacttacat acaataaaca atcttttaaa aataatgata | 1200 |
| aaacaaatga ggatctaccc agcacactga gctaatagacc caagagtgtc agggagccag | 1260 |
| ctaaatctgt ccagtgtga tactgtaggt gtgacaacac tgtgacccag cttttctgtt | 1320 |
| tgttttggtt ttttgacacg agggttctgg aggttgaact catgccttca cgcttgcagg | 1380 |
| gcaaacactt tgcagacgaa gccatctccc cagccccct cttagagtat ctccagcatg | 1440 |
| cacatcatta ggcactctac tcacaacaat ccatttatte ttcagagcaa gcccgagta | 1500 |
| ggcgacagca ctggttcccc agccccagcc tacacagtaa tcggtaagag atcagatttg | 1560 |
| aagccacata gtgttgtaag cactttcatg cgtgttaagt cgatttccaa gggacaataa | 1620 |
| gtggggaccc catttcagcc ctaccagacc tgagccccta agagtaatta ataccctacc | 1680 |
| ccgagcctga cctcttgagc aaaatttttg aaaaaaaaaat gcagatatgc tagaaaactg | 1740 |
| tatataatgt gcctaactgg ttagatttag atgaaacttg gggagattgt agaaaataag | 1800 |
| catccactat tcctatgaga tcaggaactt ggttttataa acatttatgt cattcctgtg | 1860 |
| ttagcaggaa ctctgatagg actagaggta tgaagttcag agcctttggg tagactctct | 1920 |
| gaaatcacia caggataaat ggcagaatgg gattttaaca aggtgctttg cgctccatac | 1980 |
| ccctggcaac acaggcattt tagctaactg aagaccttaa ccttccctcc ctgccagccc | 2040 |
| ttcaagtga gccacaggga cccaccagat cctatgattg ggttcctctt ctctacctaa | 2100 |

gaaataaata gctccctcag gactgatccc aagaatcaaa gctcccaaag gctcaactat 2160
 gcacagcagc atcgacctct ggcaagctgg caagaccttg gacagatttt caccttctga 2220
 ctggttcgac tgggtagtta acctacttgt gtgggtccgt actggaagtg cttggataag 2280
 aagcagagga ggaatttcaa gggataagaa agagtcctct gtgagctgtc tgccctgccct 2340
 accccaact cccaggaag gggaaagatg aactccacag tgggtggggga gaaaggtgtt 2400
 gggctatgtt ctggagttgt ggggaagggg taacctagca accactgggc tcagcatagt 2460
 cacaagcaa caggtttgcc cacaattccg acaagcctta cccttgatta gtcttctctt 2520
 ccatcttggc caggcaccag gggcttcttg ctcatatgct atagtggaca tcttcctggc 2580
 gagttcaggg ccctctcagg agggtaggga atgaaatggg atctggctcc aggtgacaac 2640
 aaaggaattg tggggggata agagggttcc tgtggttaca ttggtggctc ccttcagatc 2700
 tcttgtaact gactatcaac gagccagga tcagaggcag gggagggcag ggatgggctg 2760
 cagtgcctc atctgtctct ctctctaggt cctactgacc cttgtaggtg ggtgttgatt 2820
 cttaatctta ttgaagaatt taatggctca tgtctaacat tcatgaagaa aaaaaatcaa 2880
 gatgcaagta tactcgtaca tcttacatgt agatactgct tcagactact cccatgacca 2940
 ctgcagacac atacaggcac ggaggcatgc acgcatgcag acacacacac acacacacac 3000
 acacacacac acacacacac gaatttagac ctaaggaaaa atggatttct tgctgttgta 3060
 atggtcaaga gtgtttgaga gtttctattc taaagagcac ttttctctgt aggcgggtgg 3120
 atgagggact ttcaaagtc ctgtcttcaa gcatgaaaca tccaagaacc ccagccccta 3180
 ccatcaatga tacatgcatg gagtttcttg aagaggggagc cctgctcact ctttttagac 3240
 aaccgatcag cagcctgtga gccagatgac tatgctggcc cttgactgtg cagcctcaaa 3300
 tgaagccaac ccatcaccta ctactaacct gatgggtggg gcaccgaggc atctcagaga 3360
 gccttgcata tctgtgggtc cagcaccttt ctcaagaact acttgacca ggtcccaaac 3420
 gcttgcatag ggcctgtaga tttaaccata attctggctt tgatatctgt cgtctttcat 3480
 ccatttcttt tcatgggttt acttacaat gcactgagct gagtaagagc cacctgctca 3540
 aggaccacag caccaccact aactcatctc ctgtgtgctc tcctccttgt ccctaaaatg 3600
 ccactagggg aatgtcctta gttattttat tgtttgatct catgtttgtg ataattctgt 3660
 ttgcctggga atttgtgtgt gtgtttgggg gtggatgtgt atgagtttag gtatatgtat 3720
 gtatgggtgt gtatgagtgt gtgggtatgg tgtgtggttt tttgatgtgt ctgtatgtgt 3780
 agatgaatgt gtgagaatga gtttgtgtgt gtttgtgtat gtgtatggat gtatgtgtgt 3840
 ggtgtgtggt gtgtgtatgt gtggcaatat attgtgtatg gatgggtgtg tgtgtatgga 3900
 tgtatgtgta tgggtatgtg tgtgtatgta tgtgtatgat gtgtgtatat gagtgagtgt 3960

| | | | | | | |
|------------|-------------|-------------|-------------|------------|------------|------|
| gtgtgtgtat | ggatatgtgtg | tttatagtgt | gtggatgtgt | ggatgaatgt | gtgtgaatgg | 4020 |
| gtttgtgtgt | atgtgtagtgt | tgtgtgtgtg | tgtgtgtgtg | tgtgtgtgtg | tgtgcgcgcg | 4080 |
| cgcgcatgta | gaggtcagag | aacaacttgg | aggagttaat | tttctcttta | cctcgtgtgg | 4140 |
| gtggcaagtt | cctcagcctg | ttgagccatc | ttactgggtcc | tgtgaacttt | tacttttaaa | 4200 |
| aagcttttca | aagctgggca | tgggtgggtct | gcccttaacc | cctgactctg | gatcagacac | 4260 |
| aggtagatgt | ctgtaagttg | gagaccaagg | ttggcctggg | ctccatatca | agttccaggg | 4320 |
| cagttagggc | tacatagtga | gaccctatgc | cattgcttct | caaccttcct | aatgcggtga | 4380 |
| ccctttaata | cagtccctca | tgttgtgggtg | acccccacca | taaaattggt | tcattgcttc | 4440 |
| ttcatagctg | taattttgat | actgttatga | attgtaatgt | aactatctca | tatttgactc | 4500 |
| ctgtgagaag | gtcatttgac | cttccaaggg | gggtgcagctc | acaggttgag | aactgytccc | 4560 |
| ctgtgttgct | tccaaaccat | gccaagcact | atgtttgcat | ggtttgtcca | tgctgtggct | 4620 |
| atcactacgg | ttcactgcat | ctcattgatg | gtctgaacaa | agccccagct | ttgttagaca | 4680 |
| taggtgaaat | cactgggttt | tggctgattc | agaccctctg | aatagtgcta | ctctcccaga | 4740 |
| cagcccatgt | cacacagctg | taggagtgtc | tcttgtgtca | gggagagaaa | tggctgggtg | 4800 |
| atttgggtgc | caacttaacc | aggcactgtc | cccctctcac | tctcagatcg | catgttccag | 4860 |
| tttatacacc | cgccaccagg | ccaccagagc | tgtgccatcc | atcaaagaca | cggacattcc | 4920 |
| gagtctagtc | tttacatctc | ttattgcaaa | ccctgatatg | actacagagg | tgaaccagct | 4980 |
| gtctgagcat | cctctagtga | ggtgaggccc | taaatggaca | cgggctggag | agagcatgta | 5040 |
| agaccaaagg | ggagaggagg | caggatagaa | gacaagaata | gccttggagg | aacttggaaa | 5100 |
| aaggtgggtc | aagttccagg | gaaagccatc | taccaagggc | ctcggtagct | gtgttgacac | 5160 |
| aggtctctga | aacacagaag | gaggtagggg | tacagcagaa | gggctctgga | gtttctggag | 5220 |
| acgtctctct | tatttgggag | tagaggaagc | ctcttactgg | cacttcagag | aggtttgctt | 5280 |
| tctttcttta | agacctggat | tgcctagagc | tgaaaggaag | gagaatggaa | caggctacac | 5340 |
| agggggctgc | ccagcaacat | cttcccagca | atcagggggg | gcacgccttc | cttagcatat | 5400 |
| cccctgccc | cctccattcc | atcaggagac | ctcccaccag | ccagggccag | caagagaaga | 5460 |
| aagtgaaaaa | agccaccagg | caggtggtag | agtgcaggct | ctccttcagg | gacagacctc | 5520 |
| ggcttccttc | agggacagag | actaaacatg | gggtggcttg | ctgggaacct | gagacagctg | 5580 |
| gtctccggtc | ccaccaaga | agacaagagt | tggacgcttc | togtgtccc | tgtccgtccc | 5640 |
| ccccccccag | ctccctcccc | tttgggtcagc | ttcgctctc | ccgggaagga | ccacgtgggc | 5700 |
| aaaggactca | ctaggaccac | cctgggtcttg | gctctagttc | tgacccctgg | gtgctgaaac | 5760 |

taagataata aggacacagt cgggagggtg acagcctgaa gctgggtt

5807